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<110> AVENTIS PHARMA SA
THE GOVERNMENT OF THE UNITED STATES,

<120> NUCLEIC ACIDS OF THE HUMAN ABCC12 GENE, VECTORS
CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF

<130> ABCC12 GENE

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<141> 2002-03-05

<150> 60/272,759

<151> 2001-03-05

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<170> PatentIn Ver. 2.1

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 gaacatcctt accttcaact tggccttggt ggtgacctg agtttctcct ccatcagtac 120
 ttcacccaaa ggctgtcat tgcatacat catccag 157

<210> 25
 <211> 90
 <212> DNA
 <213> Homo sapiens

<400> 25
 ctgagcggac tgctccaagt gtgtgtgcga acgggaacag agacgcaagc caaattcacc 60

tccgtggagc tgctcagga atacatttcg

90

<210> 26
 <211> 190
 <212> DNA
 <213> Homo sapiens

<400> 26
 acctgtgttc ctgaatgcac tcatccccc aaagtgggga cctgtcccaa ggactggccc 60
 agctgtgggg agatcacctt cagagactat cagatgagat acagagacaa cccccctt 120
 gttctcgaca gcctgaactt gaacatacaa agtgggcaga cagtcgggat tggtggaaga 180
 acaggttccg 190

<210> 27
 <211> 160
 <212> DNA
 <213> Homo sapiens

<400> 27
 gaaagtcac gttaggaatg gctttgtttc gtctggtgga gccagccagt ggcacaatct 60
 ttattgatga ggtggatatc tgcattctca gcttgggaaga cctcagaacc aagctgactg 120
 tgatcccaca ggatcctgtc ctgtttgtag gtacagtaag 160

<210> 28
 <211> 79
 <212> DNA
 <213> Homo sapiens

<400> 28
 gtacaacttg gatccctttg agagtcacac cgatgagatg ctctggcagg ttctggagag 60
 aacattcatg agagacaca 79

<210> 29
 <211> 114
 <212> DNA
 <213> Homo sapiens

<400> 29
 ataatgaaac tcccagaaaa attacaggca gaagtcacag aaaatggaga aaactttctca 60
 gtagggaac gtcagctgct ttgtgtggcc cgagctcttc tccgtaattc aaag 114

<210> 30
 <211> 165
 <212> DNA
 <213> Homo sapiens

<400> 30
 atcattctcc ttgatgaagc caccgcctct atggactcca agactgacac cctgggttcag 60
 aacaccatca aagatgcctt caagggtgc actgtgctga ccatcgccca ccgcctcaac 120
 acagttctca actgcgatca cgtcctggtt atggaaaatg ggaag 165

<210> 31
 <211> 289
 <212> DNA
 <213> Homo sapiens

<400> 31

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ttactagcag cagaagtcag attgtagagg tcctggcggc tgattctaga ggaggaagag 120
gctctgtgag atgaatagga ggagtcttca ggaggagggg ctgtcctctc cgcaggcagc 180
cctggtcttc agccctctcc atccacggag tgagctgggg ctgaagttgt cccactgcc 240
atactcagtc catgtcaccc cacttggtgg gcttggggtt gggtctctggg 289

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<210> 32

<211> 85

<212> DNA

<213> Homo sapiens

<400> 32

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agagaggaag atgctggtat aatcg 85

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<210> 33

<211> 1356

<212> PRT

<213> Homo sapiens

<400> 33

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Arg Arg Arg Ser Phe Ala Glu Arg Tyr Asp Pro Ser Leu Lys Thr Met
      20              25              30

Ile Pro Val Arg Pro Cys Ala Arg Leu Ala Pro Asn Pro Val Asp Asp
      35              40              45

Ala Gly Leu Leu Ser Phe Ala Thr Phe Ser Trp Leu Thr Pro Val Met
      50              55              60

Val Lys Gly Tyr Arg Gln Arg Leu Thr Val Asp Thr Leu Pro Pro Leu
      65              70              75              80

Ser Thr Tyr Asp Ser Ser Asp Thr Asn Ala Lys Arg Phe Arg Val Leu
      85              90              95

Trp Asp Glu Glu Val Ala Arg Val Gly Pro Glu Lys Ala Ser Leu Ser
      100             105             110

His Val Val Trp Lys Phe Gln Arg Thr Arg Val Leu Met Asp Ile Val
      115             120             125

Ala Asn Ile Leu Cys Ile Ile Met Ala Ala Ile Gly Pro Thr Val Leu
      130             135             140

Ile His Gln Ile Leu Gln Gln Thr Glu Arg Thr Ser Gly Lys Val Trp
      145             150             155             160

Val Gly Ile Gly Leu Cys Ile Ala Leu Phe Ala Thr Glu Phe Thr Lys
      165             170             175

Val Phe Phe Trp Ala Leu Ala Trp Ala Ile Asn Tyr Arg Thr Ala Ile
      180             185             190

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Arg Leu Lys Val Ala Leu Ser Thr Leu Val Phe Glu Asn Leu Val Ser
 195 200 205
 Phe Lys Thr Leu Thr His Ile Ser Val Gly Glu Val Leu Asn Ile Leu
 210 215 220
 Ser Ser Asp Ser Tyr Ser Leu Phe Glu Ala Ala Leu Phe Cys Pro Leu
 225 230 235 240
 Pro Ala Thr Ile Pro Ile Leu Met Val Phe Cys Ala Ala Tyr Ala Phe
 245 250 255
 Phe Ile Leu Gly Pro Thr Ala Leu Ile Gly Ile Ser Val Tyr Val Ile
 260 265 270
 Phe Ile Pro Val Gln Met Phe Met Ala Lys Leu Asn Ser Ala Phe Arg
 275 280 285
 Arg Ser Ala Ile Leu Val Thr Asp Lys Arg Val Gln Thr Met Asn Glu
 290 295 300
 Phe Leu Thr Cys Ile Arg Leu Ile Lys Met Tyr Ala Trp Glu Lys Ser
 305 310 315 320
 Phe Thr Asn Thr Ile Gln Asp Ile Arg Arg Arg Glu Arg Lys Leu Leu
 325 330 335
 Glu Lys Ala Gly Phe Val Gln Ser Gly Asn Ser Ala Leu Ala Pro Ile
 340 345 350
 Val Ser Thr Ile Ala Ile Val Leu Thr Leu Ser Cys His Ile Leu Leu
 355 360 365
 Arg Arg Lys Leu Thr Ala Pro Val Ala Phe Ser Val Ile Ala Met Phe
 370 375 380
 Asn Val Met Lys Phe Ser Ile Ala Ile Leu Pro Phe Ser Ile Lys Ala
 385 390 395 400
 Met Ala Glu Ala Asn Val Ser Leu Arg Arg Met Lys Lys Ile Leu Ile
 405 410 415
 Asp Lys Ser Pro Pro Ser Tyr Ile Thr Gln Pro Glu Asp Pro Asp Thr
 420 425 430
 Val Leu Leu Leu Ala Asn Ala Thr Leu Thr Trp Glu His Glu Ala Ser
 435 440 445
 Arg Lys Ser Thr Pro Lys Lys Leu Gln Asn Gln Lys Arg His Leu Cys
 450 455 460
 Lys Lys Gln Arg Ser Glu Ala Tyr Ser Glu Arg Ser Pro Pro Ala Lys
 465 470 475 480
 Gly Ala Thr Gly Pro Glu Glu Gln Ser Asp Ser Leu Lys Ser Val Leu
 485 490 495
 His Ser Ile Ser Phe Val Val Arg Lys Gly Lys Ile Leu Gly Ile Cys
 500 505 510
 Gly Asn Val Gly Ser Gly Lys Ser Ser Leu Leu Ala Ala Leu Leu Gly

515					520					525				
Gln Met	Gln Leu	Gln Lys	Gly Val	Val Ala	Val Asn	Gly Thr	Leu Ala							
530			535		540									
Tyr Val	Ser Gln	Gln Ala	Trp Ile	Phe His	Gly Asn	Val Arg	Glu Asn							
545		550		555			560							
Ile Leu	Phe Gly	Glu Lys	Tyr Asp	His Gln	Arg Tyr	Gln His	Thr Val							
		565		570			575							
Arg Val	Cys Gly	Leu Gln	Lys Asp	Leu Ser	Asn Leu	Pro Tyr	Gly Asp							
	580			585			590							
Leu Thr	Glu Ile	Gly Glu	Arg Gly	Leu Asn	Leu Ser	Gly Gly	Gln Arg							
	595		600			605								
Gln Arg	Ile Ser	Leu Ala	Arg Ala	Val Tyr	Ser Asp	Arg Gln	Leu Tyr							
610			615		620									
Leu Leu	Asp Asp	Pro Leu	Ser Ala	Val Asp	Ala His	Val Gly	Lys His							
625		630		635			640							
Val Phe	Glu Glu	Cys Ile	Lys Lys	Thr Leu	Arg Gly	Lys Thr	Val Val							
		645		650			655							
Leu Val	Thr His	Gln Leu	Gln Phe	Leu Glu	Ser Cys	Asp Glu	Val Ile							
	660		665			670								
Leu Leu	Glu Asp	Gly Glu	Ile Cys	Glu Lys	Gly Thr	His Lys	Glu Leu							
	675		680			685								
Met Glu	Glu Arg	Gly Arg	Tyr Ala	Lys Leu	Ile His	Asn Leu	Arg Gly							
690			695		700									
Leu Gln	Phe Lys	Asp Pro	Glu His	Leu Tyr	Asn Ala	Ala Met	Val Glu							
705		710		715			720							
Ala Phe	Lys Glu	Ser Pro	Ala Glu	Arg Glu	Glu Asp	Ala Val	Leu Ala							
		725		730			735							
Pro Gly	Asn Glu	Lys Asp	Glu Gly	Lys Glu	Ser Glu	Thr Gly	Ser Glu							
	740		745			750								
Phe Val	Asp Thr	Lys Val	Pro Glu	His Gln	Leu Ile	Gln Thr	Glu Ser							
	755		760			765								
Pro Gln	Glu Gly	Thr Val	Thr Trp	Lys Thr	Tyr His	Thr Tyr	Ile Lys							
	770		775		780									
Ala Ser	Gly Gly	Tyr Leu	Leu Ser	Leu Phe	Thr Val	Phe Leu	Phe Leu							
785		790		795			800							
Leu Met	Ile Gly	Ser Ala	Ala Phe	Ser Asn	Trp Trp	Leu Gly	Leu Trp							
		805		810			815							
Leu Asp	Lys Gly	Ser Arg	Met Thr	Cys Gly	Pro Gln	Gly Asn	Arg Thr							
	820		825			830								
Met Cys	Glu Val	Gly Ala	Val Leu	Ala Asp	Ile Gly	Gln His	Val Tyr							
	835		840			845								

Gln Trp Val Tyr Thr Ala Ser Met Val Phe Met Leu Val Phe Gly Val
 850 855 860
 Thr Lys Gly Phe Val Phe Thr Lys Thr Thr Leu Met Ala Ser Ser Ser
 865 870 875 880
 Leu His Asp Thr Val Phe Asp Lys Ile Leu Lys Ser Pro Met Ser Phe
 885 890 895
 Phe Asp Thr Thr Pro Thr Gly Arg Leu Met Asn Arg Phe Ser Lys Asp
 900 905 910
 Met Asp Glu Leu Asp Val Arg Leu Pro Phe His Ala Glu Asn Phe Leu
 915 920 925
 Gln Gln Phe Phe Met Val Val Phe Ile Leu Val Ile Leu Ala Ala Val
 930 935 940
 Phe Pro Ala Val Leu Leu Val Val Ala Ser Leu Ala Val Gly Phe Phe
 945 950 955 960
 Ile Leu Leu Arg Ile Phe His Arg Gly Val Gln Glu Leu Lys Lys Val
 965 970 975
 Glu Asn Val Ser Arg Ser Pro Trp Phe Thr His Ile Thr Ser Ser Met
 980 985 990
 Gln Gly Leu Gly Ile Ile His Ala Tyr Gly Lys Lys Glu Ser Cys Ile
 995 1000 1005
 Thr Tyr His Leu Leu Tyr Phe Asn Cys Ala Leu Arg Trp Phe Ala Leu
 1010 1015 1020
 Arg Met Asp Val Leu Met Asn Ile Leu Thr Phe Thr Val Ala Leu Leu
 1025 1030 1035 1040
 Val Thr Leu Ser Phe Ser Ser Ile Ser Thr Ser Ser Lys Gly Leu Ser
 1045 1050 1055
 Leu Ser Tyr Ile Ile Gln Leu Ser Gly Leu Leu Gln Val Cys Val Arg
 1060 1065 1070
 Thr Gly Thr Glu Thr Gln Ala Lys Phe Thr Ser Val Glu Leu Leu Arg
 1075 1080 1085
 Glu Tyr Ile Ser Thr Cys Val Pro Glu Cys Thr His Pro Leu Lys Val
 1090 1095 1100
 Gly Thr Cys Pro Lys Asp Trp Pro Ser Cys Gly Glu Ile Thr Phe Arg
 1105 1110 1115 1120
 Asp Tyr Gln Met Arg Tyr Arg Asp Asn Thr Pro Leu Val Leu Asp Ser
 1125 1130 1135
 Leu Asn Leu Asn Ile Gln Ser Gly Gln Thr Val Gly Ile Val Gly Arg
 1140 1145 1150
 Thr Gly Ser Gly Lys Ser Ser Leu Gly Met Ala Leu Phe Arg Leu Val
 1155 1160 1165

Glu Pro Ala Ser Gly Thr Ile Phe Ile Asp Glu Val Asp Ile Cys Ile
 1170 1175 1180
 Leu Ser Leu Glu Asp Leu Arg Thr Lys Leu Thr Val Ile Pro Gln Asp
 1185 1190 1195 1200
 Pro Val Leu Phe Val Gly Thr Val Arg Tyr Asn Leu Asp Pro Phe Glu
 1205 1210 1215
 Ser His Thr Asp Glu Met Leu Trp Gln Val Leu Glu Arg Thr Phe Met
 1220 1225 1230
 Arg Asp Thr Ile Met Lys Leu Pro Glu Lys Leu Gln Ala Glu Val Thr
 1235 1240 1245
 Glu Asn Gly Glu Asn Phe Ser Val Gly Glu Arg Gln Leu Leu Cys Val
 1250 1255 1260
 Ala Arg Ala Leu Leu Arg Asn Ser Lys Ile Ile Leu Leu Asp Glu Ala
 1265 1270 1275 1280
 Thr Ala Ser Met Asp Ser Lys Thr Asp Thr Leu Val Gln Asn Thr Ile
 1285 1290 1295
 Lys Asp Ala Phe Lys Gly Cys Thr Val Leu Thr Ile Ala His Arg Leu
 1300 1305 1310
 Asn Thr Val Leu Asn Cys Asp His Val Leu Val Met Glu Asn Gly Lys
 1315 1320 1325
 Val Ile Glu Phe Asp Lys Pro Glu Val Leu Ala Glu Lys Pro Asp Ser
 1330 1335 1340
 Ala Phe Ala Met Leu Leu Ala Ala Glu Val Arg Leu
 1345 1350 1355

<210> 34
 <211> 1359
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Val Gly Glu Gly Pro Tyr Leu Ile Ser Asp Leu Asp Gln Arg Gly
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 Ile Pro Val Arg Pro Cys Ala Arg Leu Ala Pro Asn Pro Val Asp Asp
 35 40 45
 Ala Gly Leu Leu Ser Phe Ala Thr Phe Ser Trp Leu Thr Pro Val Met
 50 55 60
 Val Lys Gly Tyr Arg Gln Arg Leu Thr Val Asp Thr Leu Pro Pro Leu
 65 70 75 80
 Ser Thr Tyr Asp Ser Ser Asp Thr Asn Ala Lys Arg Phe Arg Val Leu
 85 90 95

Trp Asp Glu Glu Val Ala Arg Val Gly Pro Glu Lys Ala Ser Leu Ser
 100 105 110
 His Val Val Trp Lys Phe Gln Arg Thr Arg Val Leu Met Asp Ile Val
 115 120 125
 Ala Asn Ile Leu Cys Ile Ile Met Ala Ala Ile Gly Pro Thr Val Leu
 130 135 140
 Ile His Gln Ile Leu Gln Gln Thr Glu Arg Thr Ser Gly Lys Val Trp
 145 150 155 160
 Val Gly Ile Gly Leu Cys Ile Ala Leu Phe Ala Thr Glu Phe Thr Lys
 165 170 175
 Val Phe Phe Trp Ala Leu Ala Trp Ala Ile Asn Tyr Arg Thr Ala Ile
 180 185 190
 Arg Leu Lys Val Ala Leu Ser Thr Leu Val Phe Glu Asn Leu Val Ser
 195 200 205
 Phe Lys Thr Leu Thr His Ile Ser Val Gly Glu Val Leu Asn Ile Leu
 210 215 220
 Ser Ser Asp Ser Tyr Ser Leu Phe Glu Ala Ala Leu Phe Cys Pro Leu
 225 230 235 240
 Pro Ala Thr Ile Pro Ile Leu Met Val Phe Cys Ala Ala Tyr Ala Phe
 245 250 255
 Phe Ile Leu Gly Pro Thr Ala Leu Ile Gly Ile Ser Val Tyr Val Ile
 260 265 270
 Phe Ile Pro Val Gln Met Phe Met Ala Lys Leu Asn Ser Ala Phe Arg
 275 280 285
 Arg Ser Ala Ile Leu Val Thr Asp Lys Arg Val Gln Thr Met Asn Glu
 290 295 300
 Phe Leu Thr Cys Ile Arg Leu Ile Lys Met Tyr Ala Trp Glu Lys Ser
 305 310 315 320
 Phe Thr Asn Thr Ile Gln Asp Ile Arg Arg Arg Glu Arg Lys Leu Leu
 325 330 335
 Glu Lys Ala Gly Phe Val Gln Ser Gly Asn Ser Ala Leu Ala Pro Ile
 340 345 350
 Val Ser Thr Ile Ala Ile Val Leu Thr Leu Ser Cys His Ile Leu Leu
 355 360 365
 Arg Arg Lys Leu Thr Ala Pro Val Ala Phe Ser Val Ile Ala Met Phe
 370 375 380
 Asn Val Met Lys Phe Ser Ile Ala Ile Leu Pro Phe Ser Ile Lys Ala
 385 390 395 400
 Met Ala Glu Ala Asn Val Ser Leu Arg Arg Met Lys Lys Ile Leu Ile
 405 410 415

Asp Lys Ser Pro Pro Ser Tyr Ile Thr Gln Pro Glu Asp Pro Asp Thr
 420 425 430
 Val Leu Leu Leu Ala Asn Ala Thr Leu Thr Trp Glu His Glu Ala Ser
 435 440 445
 Arg Lys Ser Thr Pro Lys Lys Leu Gln Asn Gln Lys Arg His Leu Cys
 450 455 460
 Lys Lys Gln Arg Ser Glu Ala Tyr Ser Glu Arg Ser Pro Pro Ala Lys
 465 470 475 480
 Gly Ala Thr Gly Pro Glu Glu Gln Ser Asp Ser Leu Lys Ser Val Leu
 485 490 495
 His Ser Ile Ser Phe Val Val Arg Lys Gly Lys Ile Leu Gly Ile Cys
 500 505 510
 Gly Asn Val Gly Ser Gly Lys Ser Ser Leu Leu Ala Ala Leu Leu Gly
 515 520 525
 Gln Met Gln Leu Gln Lys Gly Val Val Ala Val Asn Gly Thr Leu Ala
 530 535 540
 Tyr Val Ser Gln Gln Ala Trp Ile Phe His Gly Asn Val Arg Glu Asn
 545 550 555 560
 Ile Leu Phe Gly Glu Lys Tyr Asp His Gln Arg Tyr Gln His Thr Val
 565 570 575
 Arg Val Cys Gly Leu Gln Lys Asp Leu Ser Asn Leu Pro Tyr Gly Asp
 580 585 590
 Leu Thr Glu Ile Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Arg
 595 600 605
 Gln Arg Ile Ser Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Leu Tyr
 610 615 620
 Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His
 625 630 635 640
 Val Phe Glu Glu Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val
 645 650 655
 Leu Val Thr His Gln Leu Gln Phe Leu Glu Ser Cys Asp Glu Val Ile
 660 665 670
 Leu Leu Glu Asp Gly Glu Ile Cys Glu Lys Gly Thr His Lys Glu Leu
 675 680 685
 Met Glu Glu Arg Gly Arg Tyr Ala Lys Leu Ile His Asn Leu Arg Gly
 690 695 700
 Leu Gln Phe Lys Asp Pro Glu His Leu Tyr Asn Ala Ala Met Val Glu
 705 710 715 720
 Ala Phe Lys Glu Ser Pro Ala Glu Arg Glu Glu Asp Ala Gly Ile Ile
 725 730 735
 Val Leu Ala Pro Gly Asn Glu Lys Asp Glu Gly Lys Glu Ser Glu Thr

740	745	750
Gly Ser Glu Phe Val Asp Thr Lys Val Pro Glu His Gln Leu Ile Gln 755	760	765
Thr Glu Ser Pro Gln Glu Gly Thr Val Thr Trp Lys Thr Tyr His Thr 770	775	780
Tyr Ile Lys Ala Ser Gly Gly Tyr Leu Leu Ser Leu Phe Thr Val Phe 785	790	795 800
Leu Phe Leu Leu Met Ile Gly Ser Ala Ala Phe Ser Asn Trp Trp Leu 805	810	815
Gly Leu Trp Leu Asp Lys Gly Ser Arg Met Thr Cys Gly Pro Gln Gly 820	825	830
Asn Arg Thr Met Cys Glu Val Gly Ala Val Leu Ala Asp Ile Gly Gln 835	840	845
His Val Tyr Gln Trp Val Tyr Thr Ala Ser Met Val Phe Met Leu Val 850	855	860
Phe Gly Val Thr Lys Gly Phe Val Phe Thr Lys Thr Thr Leu Met Ala 865	870	875 880
Ser Ser Ser Leu His Asp Thr Val Phe Asp Lys Ile Leu Lys Ser Pro 885	890	895
Met Ser Phe Phe Asp Thr Thr Pro Thr Gly Arg Leu Met Asn Arg Phe 900	905	910
Ser Lys Asp Met Asp Glu Leu Asp Val Arg Leu Pro Phe His Ala Glu 915	920	925
Asn Phe Leu Gln Gln Phe Phe Met Val Val Phe Ile Leu Val Ile Leu 930	935	940
Ala Ala Val Phe Pro Ala Val Leu Leu Val Val Ala Ser Leu Ala Val 945	950	955 960
Gly Phe Phe Ile Leu Leu Arg Ile Phe His Arg Gly Val Gln Glu Leu 965	970	975
Lys Lys Val Glu Asn Val Ser Arg Ser Pro Trp Phe Thr His Ile Thr 980	985	990
Ser Ser Met Gln Gly Leu Gly Ile Ile His Ala Tyr Gly Lys Lys Glu 995	1000	1005
Ser Cys Ile Thr Tyr His Leu Leu Tyr Phe Asn Cys Ala Leu Arg Trp 1010	1015	1020
Phe Ala Leu Arg Met Asp Val Leu Met Asn Ile Leu Thr Phe Thr Val 1025	1030	1035 1040
Ala Leu Leu Val Thr Leu Ser Phe Ser Ser Ile Ser Thr Ser Ser Lys 1045	1050	1055
Gly Leu Ser Leu Ser Tyr Ile Ile Gln Leu Ser Gly Leu Leu Gln Val 1060	1065	1070

Cys Val Arg Thr Gly Thr Glu Thr Gln Ala Lys Phe Thr Ser Val Glu
 1075 1080 1085

Leu Leu Arg Glu Tyr Ile Ser Thr Cys Val Pro Glu Cys Thr His Pro
 1090 1095 1100

Leu Lys Val Gly Thr Cys Pro Lys Asp Trp Pro Ser Cys Gly Glu Ile
 1105 1110 1115 1120

Thr Phe Arg Asp Tyr Gln Met Arg Tyr Arg Asp Asn Thr Pro Leu Val
 1125 1130 1135

Leu Asp Ser Leu Asn Leu Asn Ile Gln Ser Gly Gln Thr Val Gly Ile
 1140 1145 1150

Val Gly Arg Thr Gly Ser Gly Lys Ser Ser Leu Gly Met Ala Leu Phe
 1155 1160 1165

Arg Leu Val Glu Pro Ala Ser Gly Thr Ile Phe Ile Asp Glu Val Asp
 1170 1175 1180

Ile Cys Ile Leu Ser Leu Glu Asp Leu Arg Thr Lys Leu Thr Val Ile
 1185 1190 1195 1200

Pro Gln Asp Pro Val Leu Phe Val Gly Thr Val Arg Tyr Asn Leu Asp
 1205 1210 1215

Pro Phe Glu Ser His Thr Asp Glu Met Leu Trp Gln Val Leu Glu Arg
 1220 1225 1230

Thr Phe Met Arg Asp Thr Ile Met Lys Leu Pro Glu Lys Leu Gln Ala
 1235 1240 1245

Glu Val Thr Glu Asn Gly Glu Asn Phe Ser Val Gly Glu Arg Gln Leu
 1250 1255 1260

Leu Cys Val Ala Arg Ala Leu Leu Arg Asn Ser Lys Ile Ile Leu Leu
 1265 1270 1275 1280

Asp Glu Ala Thr Ala Ser Met Asp Ser Lys Thr Asp Thr Leu Val Gln
 1285 1290 1295

Asn Thr Ile Lys Asp Ala Phe Lys Gly Cys Thr Val Leu Thr Ile Ala
 1300 1305 1310

His Arg Leu Asn Thr Val Leu Asn Cys Asp His Val Leu Val Met Glu
 1315 1320 1325

Asn Gly Lys Val Ile Glu Phe Asp Lys Pro Glu Val Leu Ala Glu Lys
 1330 1335 1340

Pro Asp Ser Ala Phe Ala Met Leu Leu Ala Ala Glu Val Arg Leu
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<210> 35

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 35

tccttcgcca cattttcc

18

<210> 36

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 36

attgagcacc tcgccaac

18

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 37

ttctcattca ccaaatcctc c

21

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 38

acattaaaca tggcaatcac ac

22

<210> 39

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 39

gtgtgattgc catgtttaat gt

22

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 40

ggagtgcatt aagaagacgc

20

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 41

cagagaggag gatgccat

18

<210> 42

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 42

cactgcaagc atggtgttc

19

<210> 43

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 43

ctcatcggtg tgactctca

19

<210> 44

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 44

tttgagagtc acaccgatga gat

23

<210> 45

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 45

cccagaacca accccaag

18

<210> 46

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 46

ggctctgtga gatgaatagg

20